

**Exhibit A**

**Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 10/041,770**

1. (Amended) An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1.
2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO:2; and
  - (b) hybridizes to the nucleotide sequence of SEQ ID NO:1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence described in SEQ ID NO:2.
4. (Amended) An isolated expression vector comprising a nucleic acid molecule that comprises the nucleotide sequence of SEQ ID NO:1.
5. (New) An isolated expression vector comprising a nucleic acid molecule that encodes the amino acid sequence described in SEQ ID NO:2.
6. (New) A host cell comprising the expression vector of claim 4 or 5.

**Exhibit A**

**Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 10/041,770**

1. (Amended) An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1.
2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO:2; and
  - (b) hybridizes to the nucleotide sequence of SEQ ID NO:1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence described in SEQ ID NO:2.
4. (Amended) An isolated expression vector comprising a nucleic acid molecule that comprises the nucleotide sequence of SEQ ID NO:1.
5. (New) An isolated expression vector comprising a nucleic acid molecule that encodes the amino acid sequence described in SEQ ID NO:2.
6. (New) A host cell comprising the expression vector of claim 4 or 5.

**Exhibit B**

**Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 10/041,770**

1. (Amended) An isolated nucleic acid molecule comprising [at least 60 contiguous nucleotides from] the nucleotide sequence of SEQ ID NO:1.
2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO:2; and
  - (b) hybridizes [under highly stringent conditions] to the nucleotide sequence of SEQ ID NO:1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence described in SEQ ID NO:2.
4. (Amended) An isolated expression vector comprising a nucleic acid molecule that comprises [at least 60 contiguous nucleotides from] the nucleotide sequence of SEQ ID NO:1.
5. (New) An isolated expression vector comprising a nucleic acid molecule that encodes the amino acid sequence described in SEQ ID NO:2.
6. (New) A host cell comprising the expression vector of claim 4 or 5.

Query= SEQ ID NO:1  
(2634 letters)



Sequences producing significant alignments:

Score (bits)	E Value
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AL356356.17.1.176550 1386 0.0

>AL356356 ACCESSION:AL356356 NID: gi 18476570 emb AL356356.17 Human DNA sequence from clone RP11-54A4 on chromosome 1, complete sequence

Length = 176550

Identities = 699/699 (100%)

Strand = Plus / Plus

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|||||||

Query: 493 gcattgccactgcaccggaaccgcaggcaccctcgagccacccagatctgagctgtcc 552  
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|||||||

Query: 553 ctgatctttctagagggaaagaggctattccgtccctactccaagagcagagccattc 612  
|||||||

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|||||||

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Strand = Plus / Plus

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Query: 377 gaggtcccgcttcccaccttagggagagaggagaccaggagattcgagcggccaggaggt 436  
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Identities = 252/255 (98%)

Strand = Plus / Plus

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Query: 2440 aacggtgatgaagtgagcgagcaggagtgtcgctcaggccccccacagccccccAGCAGA 2499

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Strand = Plus / Plus

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Sbjct: 83543 cctggctatcagaagatcttggatccagcggagcctgcggctccagattGCCA 83602

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Strand = Plus / Plus

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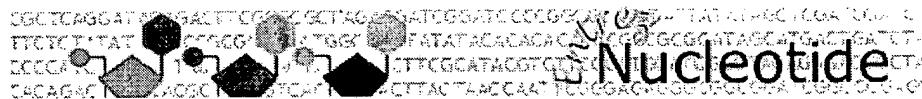
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Strand = Plus / Plus

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PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

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default

Show: 20

Send to

File

Get Subsequence

1: AL356356. Human DNA sequenc...[gi:18476570]

Links

**LOCUS** AL356356 176550 bp DNA linear PRI 30-JAN-2002  
**DEFINITION** Human DNA sequence from clone RP11-54A4 on chromosome 1, complete sequence.  
**ACCESSION** AL356356  
**VERSION** AL356356.17 GI:18476570  
**KEYWORDS** HTG.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 176550)  
**AUTHORS** Heath, P.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
**COMMENT** On Feb 1, 2002 this sequence version replaced gi:18250748.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr1>  
RP11-54A4 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
**VECTOR:** pBACe3.6  
**IMPORTANT:** This sequence is not the entire insert of clone RP11-54A4. It may be shorter because we sequence overlapping sections only once, except for a short overlap.  
The true left end of clone RP11-54A4 is at 1 in this sequence. The

>NM\_019032 ACCESSION:NM\_019032 NID: gi 24308134 ref NM\_019032.1  
Homo sapiens thrombospondin repeat containing 1 (TSRC1),  
mRNA  
Length = 2704

Score = 950 bits (2428), Expect = 0.0  
Identities = 431/433 (99%), Positives = 431/433 (99%)  
Frame = +1

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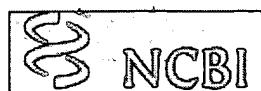
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Query: 845 WFHSDWSSKVSPE 857  
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Sequence Viewer

Search **Nucleotide** for

Limits Preview/Index History Clipboard Details

Display default Show: 20

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 VERSION NM\_019032.1 GI:24308134  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2704)  
 AUTHORS Strausberg, R.  
 TITLE Homo sapiens, hypothetical protein, clone MGC:34896 IMAGE:5001173,  
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 JOURNAL Unpublished (2002)  
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final  
 NCBI review. The reference sequence was derived from BC027478.1.  
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variation complement(2167)  
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Jun 19 2003 12:37:45

>AY158701 ACCESSION:AY158701 NID: gi 30024980 gb AY158701.1 Mus  
musculus thrombospondin repeat protein 1 (Tsrc1) mRNA,  
complete cds  
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Frame = +3

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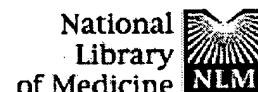
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PMC

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OMIM

Bc

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1: Gene. 2003 Mar 27;307:23-30.

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## TSRC1, a widely expressed gene containing seven thrombospondin type I repeats.

Buchner DA, Meisler MH.

Department of Human Genetics, University of Michigan School of Medicine  
 Ann Arbor, MI 48109-0618, USA.

The thrombospondin type 1 repeat domain is found in nearly 100 mammalian proteins with diverse biological functions that include cellular adhesion, angiogenesis, and patterning of the developing nervous system. We have characterized a novel thrombospondin type 1 repeat containing gene, TSRC1 encoding a predicted protein with seven thrombospondin repeats, six of which are clustered at the C-terminus. The 17 coding exons and two nontranslated exons of TSRC1 span 10 kb of genomic DNA. The human and mouse genes encode proteins of 1074 and 1036 amino acids, respectively, with 76% amino acid sequence identity. Thirty of the extra amino acids in the human protein are encoded by exon 6. Mouse *Tsrc1* is expressed in all fetal and adult tissues tested. Three conserved noncoding sequence elements with potential regulatory function are located in intron 1. Mouse *Tsrc1* was genetically mapped to chromosome 3 within the nonrecombinant region for the sodium channel modifier locus *Scnm1*. The sensitive and resistant alleles of *Scnm1* did not differ in *Tsrc1* protein sequence, transcript length, or transcript abundance. Human TSRC1 is located on chromosome 1q21 within an 11.7 Mb segment of conserved synteny. TSRC1 and the closely linked gene ADAM15 appear to be derived by a chromosomal inversion that interrupted an ancestral ADAMTS gene.

PMID: 12706885 [PubMed - indexed for MEDLINE]

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## **SMART ANALYSIS**

Domains within the query sequence of 877 residues

